



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/768,932

Source: IFwo

Date Processed by STIC: 2/10/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 101760, 132

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 _____ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 _____ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 _____ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 _____ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 _____ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 _____ Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 _____ Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 _____ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 _____ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 _____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 _____ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 _____ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 03/10/2004

PATENT APPLICATION: US/10/768,932

TIME: 10:17:23

Input Set : N:\Crf4\Refhold\10_folder\J768932.raw

Output Set: N:\CRF4\03092004\J768932.raw

1 <110> APPLICANT: Glass, David J.
 2 Karow, Margaret
 3 Smith, Eric
 4 <120> TITLE OF INVENTION: HIV-Specific Fusion Proteins and
 5 Therapeutic and Diagnostic Methods For Use
 6 <130> FILE REFERENCE: REG 990A
 7 <140> CURRENT APPLICATION NUMBER: US/10/768,932
 8 <141> CURRENT FILING DATE: 2004-01-30
 9 <150> PRIOR APPLICATION NUMBER: US 60/446,347
 10 <151> PRIOR FILING DATE: 2003-02-10
 11 <160> NUMBER OF SEQ ID NOS: 18
 12 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 446
 16 <212> TYPE: PRT
 17 <213> ORGANISM: Artificial Sequence
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: Artificial Constructs
 20 <400> SEQUENCE: 1

21	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr	Ser
22	1				5					10					15	
23	Glu	Pro	Ser	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	Leu
24				20					25					30		
25	Thr	Arg	Gly	Gly	Ala	Ile	Ala	Lys	Lys	Val	Val	Leu	Gly	Lys	Lys	Gly
26			35					40					45			
27	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser	Ile	Gln
28		50					55					60				
29	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn	Gln	Gly
30		65			70					75					80	
31	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala	Asp	Ser
32				85					90						95	
33	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	Lys	Asn
34				100					105						110	
35	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	Asp	Gln
36			115					120					125			
37	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	Ser	Asp
38		130					135					140				
39	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	Ser	Pro
40		145				150				155					160	
41	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	Lys	Asn
42				165					170						175	
43	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu	Gln	Asp
44			180					185							190	

Does Not Comply
 Corrected Diskette Needed

*give source of genetic material
 (see item 11
 on Error
 Summary
 sheet)*

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Input Set : N:\Crf4\Refhold\10_folder\J768932.raw

Output Set: N:\CRF4\03092004\J768932.raw

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45      Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys Val Glu
46              195                      200                      205
47      Phe Lys Ile Asp Ile Val Val Leu Ala Ser Gly Asp Lys Thr His Thr
48              210                      215                      220
49      Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
50      225                      230                      235                      240
51      Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
52              245                      250                      255
53      Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
54              260                      265                      270
55      Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
56              275                      280                      285
57      Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
58              290                      295                      300
59      Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
60      305                      310                      315                      320
61      Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
62              325                      330                      335
63      Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
64              340                      345                      350
65      Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
66              355                      360                      365
67      Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
68              370                      375                      380
69      Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
70      385                      390                      395                      400
71      Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
72              405                      410                      415
73      Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
74              420                      425                      430
75      Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
76              435                      440                      445
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 450
80 <212> TYPE: PRT
81 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Artificial Constructs
84 <400> SEQUENCE: 2
85      Arg Ser Thr Arg Gly Gly Ala Ile Ala Lys Lys Val Val Leu Gly Lys
86              1              5              10              15
87      Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
88              20              25              30
89      Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
90              35              40              45
91      Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
92              50              55              60
93      Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
94      65              70              75              80

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Same env

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TIME: 10:17:23

Input Set : N:\Crf4\Refhold\10_folder\J768932.raw

Output Set: N:\CRF4\03092004\J768932.raw

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95      Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
96                      85                      90                      95
97      Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
98                      100                      105                      110
99      Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
100                     115                     120                     125
101      Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
102                     130                     135                     140
103      Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
104                     145                     150                     155                     160
105      Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
106                     165                     170                     175
107      Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Thr Arg Asp Tyr Gln
108                     180                     185                     190
109      Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr Ser Glu Pro Ser
110                     195                     200                     205
111      Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu Leu Ser Gly Asp
112                     210                     215                     220
113      Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
114                     225                     230                     235                     240
115      Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
116                     245                     250                     255
117      Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
118                     260                     265                     270
119      Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
120                     275                     280                     285
121      Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
122                     290                     295                     300
123      Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
124                     305                     310                     315                     320
125      Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
126                     325                     330                     335
127      Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
128                     340                     345                     350
129      Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
130                     355                     360                     365
131      Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
132                     370                     375                     380
133      Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
134                     385                     390                     395                     400
135      Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
136                     405                     410                     415
137      Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
138                     420                     425                     430
139      Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
140                     435                     440                     445
141      Gly Lys
142                     450
144 <210> SEQ ID NO: 3

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RAW SEQUENCE LISTING

DATE: 03/10/2004

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Input Set : N:\Crf4\Refhold\10_folder\J768932.raw

Output Set: N:\CRF4\03092004\J768932.raw

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145 <211> LENGTH: 436
146 <212> TYPE: PRT
147 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Artificial Constructs
150 <400> SEQUENCE: 3
151   Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr Ser
152     1             5             10             15
153   Glu Pro Ser Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu Leu
154             20             25             30
155   Thr Arg Gly Gly Ala Ile Ala Thr Val Glu Leu Thr Cys Thr Ala Ser
156             35             40             45
157   Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys
158             50             55             60
159   Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu
160             65             70             75             80
161   Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe
162             85             90             95
163   Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile
164             100            105            110
165   Cys Glu Val Glu Asp Gln Lys Glu Val Gln Leu Leu Val Phe Gly
166             115            120            125
167   Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr
168             130            135            140
169   Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg
170             145            150            155            160
171   Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser
172             165            170            175
173   Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln
174             180            185            190
175   Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Ser
176             195            200            205
177   Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
178             210            215            220
179   Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
180             225            230            235            240
181   Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
182             245            250            255
183   His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
184             260            265            270
185   Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
186             275            280            285
187   Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
188             290            295            300
189   Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
190             305            310            315            320
191   Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
192             325            330            335
193   Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val

```

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Input Set : N:\Crf4\Refhold\10_folder\J768932.raw

Output Set: N:\CRF4\03092004\J768932.raw

194 340 345 350
 195 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 196 355 360 365
 197 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 198 370 375 380
 199 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 200 385 390 395 400
 201 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 202 405 410 415
 203 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 204 420 425 430
 205 Ser Pro Gly Lys
 206 435
 208 <210> SEQ ID NO: 4
 209 <211> LENGTH: 621
 210 <212> TYPE: PRT
 211 <213> ORGANISM: Artificial Sequence
 212 <220> FEATURE:
 213 <223> OTHER INFORMATION: Artificial Constructs
 214 <400> SEQUENCE: 4
 215 Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr Ser
 216 1 5 10 15
 217 Glu Pro Ser Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu Leu
 218 20 25 30
 219 Thr Arg Gly Gly Ala Ile Ala Lys Lys Val Val Leu Gly Lys Lys Gly
 220 35 40 45
 221 Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser Ile Gln
 222 50 55 60
 223 Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn Gln Gly
 224 65 70 75 80
 225 Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala Asp Ser
 226 85 90 95
 227 Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile Lys Asn
 228 100 105 110
 229 Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu Asp Gln
 230 115 120 125
 231 Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn Ser Asp
 232 130 135 140
 233 Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu Ser Pro
 234 145 150 155 160
 235 Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly Lys Asn
 236 165 170 175
 237 Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu Gln Asp
 238 180 185 190
 239 Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys Val Glu
 240 195 200 205
 241 Phe Lys Ile Asp Ile Val Val Leu Ala Ser Gly Phe Gln Lys Ala Ser
 242 210 215 220
 243 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

DATE: 03/10/2004

PATENT APPLICATION: US/10/768,932

TIME: 10:17:24

Input Set : N:\Crf4\Refhold\10_folder\J768932.raw

Output Set: N:\CRF4\03092004\J768932.raw